

## 43072-0002PC.TXT

## SEQUENCE LISTING

<110> ExSAR Corporation  
Mark Robert Southern  
Yoshitomo Hamuro  
Patrick Robert Griffin

<120> Drug Candidate Selection by Hydrogen  
Exchange Characterization of Ligand-Induced Receptor  
Conformation

<130> 43072-0002 PC

<160> 2

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 266

<212> PRT

<213> Artificial Sequence

<220>

<223> Homo sapiens PPAR gamma ligand binding domain

<400> 1

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Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu
 35      40      45
Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys
 50      55      60
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu
 65      70      75      80
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val
 85      90      95
Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His
100      105      110
Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val
115      120      125
Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser
130      135      140
Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala
145      150      155      160
Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe
165      170      175
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
180      185      190
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu
195      200      205
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu
210      215      220
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln
225      230      235      240
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Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
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<210> 2

<211> 505

<212> PRT

<213> Homo sapiens

&lt;220&gt;

&lt;400&gt; 2

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 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val  
 35 40 45  
 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
 50 55 60  
 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
 65 70 75 80  
 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
 85 90 95  
 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
 100 105 110  
 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
 115 120 125  
 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
 130 135 140  
 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
 145 150 155 160  
 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
 165 170 175  
 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
 180 185 190  
 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile  
 195 200 205  
 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu  
 210 215 220  
 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg  
 225 230 235 240  
 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu  
 245 250 255  
 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys  
 260 265 270  
 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp  
 275 280 285  
 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu  
 290 295 300  
 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala  
 305 310 315 320  
 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn  
 325 330 335  
 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu  
 340 345 350  
 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu  
 355 360 365  
 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu  
 370 375 380  
 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val  
 385 390 395 400  
 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile  
 405 410 415  
 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys  
 420 425 430  
 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln  
 435 440 445  
 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu  
 450 455 460  
 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu  
 465 470 475 480  
 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu  
 485 490 495  
 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
 500 505

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